



SEQUENCE LISTING

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TECH CENTER 1600/2900

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Hernstadt, Corinna
Wilcox, Edward R.
Wong, Siu-Yin

<120> Process for Altering the Host Range of *Bacillus thuringiensis* Toxins, and Novel Toxins Produced Thereby

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<140> US 10/035,060

<141> 2001-12-27

<150> US 09/405,788

<151> 1999-09-27

<150> US 08/855,160

<151> 1997-05-13

<150> US 08/580,781

<151> 1995-12-29

<150> US 08/420,615

<151> 1995-04-10

<150> US 08/097,808

<151> 1993-07-27

<150> US 07/980,128

<151> 1992-11-23

<150> US 07/803,920

<151> 1991-12-06

<150> US 07/356,599

<151> 1989-05-24

<150> US 06/904,572

<151> 1986-09-05

<150> US 06/808,129

<151> 1985-12-12

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<170> PatentIn version 3.1

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Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
 50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
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Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
 85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
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Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
 115 120 125

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Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
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Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
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Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Trp Ser Gly His Gln
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Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
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Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
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Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
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Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
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Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
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Arg Ala Pro Thr Phe Ser Trp Gln His Arg Ser Ala Glu Phe Asn Asn
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Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
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Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
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Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
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Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
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Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
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Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
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Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
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Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
580 585 590

Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
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Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val
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Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
625 630 635 640

Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser
645 650 655

Asp Glu Phe Cys Leu Asp Glu Lys Gln Glu Leu Ser Glu Lys Val Lys
660 665 670

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn
675 680 685

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr
690 695 700

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
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Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
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Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
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Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
755 760 765

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785 790 795 800

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Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
820 825 830

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Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu
885 890 895

Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
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Val Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala Met
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Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu
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Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val
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Lys Gly His Val Asp Val Glu Glu Gln Asn Asn Gln Arg Ser Val Leu
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Val Leu Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val
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Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu
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 Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Pro Val Gln Ile
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 Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
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Gln Asn Ile Arg Gln Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
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Ile Tyr Thr Asp Val His Arg Gly Phe Asn Tyr Trp Ser Gly His Gln
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Thr Gly Leu Gly Ile Phe Arg Thr Leu Ser Ser Pro Leu Tyr Arg Arg
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Gly Thr Glu Phe Ser Phe Ala Ser Leu Thr Thr Asn Leu Pro Ser Thr
385 390 395 400

Ile Tyr Arg Gln Arg Gly Thr Val Asp Ser Leu Asp Val Ile Pro Pro
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Gln Asp Asn Ser Val Pro Pro Arg Ala Gly Phe Ser His Arg Leu Ser
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His Val Thr Met Leu Ser Gln Ala Ala Gly Ala Val Tyr Thr Leu Arg
435 440 445

Ala Gln Arg Pro Met Phe Ser Trp Ile His Arg Ser Ala Glu Phe Asn
450 455 460

Asn Ile Ile Ala Ser Asp Ser Ile Thr Gln Ile Pro Ala Val Lys Gly
 465 470 475 480
 Asn Phe Leu Phe Asn Gly Ser Val Ile Ser Gly Pro Gly Phe Thr Gly
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 Gly Asp Leu Val Arg Leu Asn Ser Ser Gly Asn Asn Ile Gln Asn Arg
 500 505 510
 Gly Tyr Ile Glu Val Pro Ile His Phe Pro Ser Thr Ser Thr Arg Tyr
 515 520 525
 Arg Val Arg Val Arg Tyr Ala Ser Val Thr Pro Ile His Leu Asn Val
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 Asn Trp Gly Asn Ser Ser Ile Phe Ser Asn Thr Val Pro Ala Thr Ala
 545 550 555 560
 Thr Ser Leu Asp Asn Leu Gln Ser Ser Asp Phe Gly Tyr Phe Glu Ser
 565 570 575
 Ala Asn Ala Phe Thr Ser Ser Leu Gly Asn Ile Val Gly Val Arg Asn
 580 585 590
 Phe Ser Gly Thr Ala Gly Val Ile Ile Asp Arg Phe Glu Phe Ile Pro
 595 600 605
 Val Thr Ala Thr Leu Glu Ala Glu Tyr Asn Leu Glu Arg Ala Gln Lys
 610 615 620
 Ala Val Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly Leu Lys Thr
 625 630 635 640
 Asn Val Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Thr Tyr
 645 650 655
 Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys
 660 665 670
 Val Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp
 675 680 685
 Ser Asn Phe Lys Asp Ile Asn Arg Gln Pro Glu Arg Gly Trp Gly Gly
 690 695 700
 Ser Thr Gly Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn
 705 710 715 720
 Tyr Val Thr Leu Ser Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu
 725 730 735
 Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys Ala Phe Thr Arg Tyr Gln
 740 745 750
 Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile
 755 760 765

Arg Tyr Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser
770 775 780

Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro
785 790 795 800

Asn Arg Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser
805 810 815

Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu
820 825 830

Asp Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp
835 840 845

Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn
850 855 860

Leu Glu Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg
865 870 875 880

Val Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu
885 890 895

Trp Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala
900 905 910

Leu Phe Val Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile
915 920 925

Ala Met Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala
930 935 940

Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe
945 950 955 960

Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala
965 970 975

Arg Asn Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp
980 985 990

Asn Val Lys Gly His Val Asp Val Glu Glu Gln Asn Asn Gln Arg Ser
995 1000 1005

Val Leu Val Val Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val
1010 1015 1020

Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr
1025 1030 1035

Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu
1040 1045 1050

Asn Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu
1055 1060 1065

Ile Tyr Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Val Asn
 1070 1075 1080

Gln Glu Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn Arg Gly Tyr
 1085 1090 1095

Asn Glu Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu
 1100 1105 1110

Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys Glu Phe
 1115 1120 1125

Asn Arg Gly Tyr Arg Asp Tyr Thr Pro Leu Pro Val Gly Tyr Val
 1130 1135 1140

Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 1145 1150 1155

Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu
 1160 1165 1170

Leu Leu Leu Met Glu Glu
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<211> 3531
<212> DNA
<213> *Bacillus thuringiensis*

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tgcgttaacgc aatttccttt gagtgaattt gttcccggtg ctggatttgt gttaggacta	180
gttgatataa tatggggaat ttttggtccc tctcaatggg acgcatttct tgtacaaatt	240
gaacagttaa ttaaccaaag aatagaagaa ttccgcttagga accaagccat ttctagatta	300
gaaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagagtg ggaagcagat	360
cctactaattc cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgcc	420
cttacaaccc ctattcctct ttttgcagtt caaaatttac aagttcctct tttatcagta	480
tatgttcaag ctgcaaattt acatttatca gttttgagag atgtttcagt gtttggacaa	540
aggccccat ttgatgccgc gactatcaat agtcgttata atgatttaac taggcttatt	600
ggcaactata cagattatgc tgtacgctgg tacaatacgg gattagaacg tgtatgggaa	660
ccggattcta gagattgggt aaggtataat caatttagaa gagaattaac actaactgta	720
ttagatatcg ttgctctgtt cccgaattat gatagtagaa gatatccaat tcgaacagtt	780

tcccaattaa caagagaaaat ttatacaaacc ccagtattttgaaaatggtagttt	840
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aacagtataaa ccatctatac ggatgctcat aggggttattt attattggtc agggcatcaa	960
ataatggctt ctccgttagg gtttcgggg ccagaattca ctttccgct atatggaact	1020
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ctggatgaaa aacaagaatt gtccgagaaa gtcaaaccatg cgaagcgact tagtgatgag	2040
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 gagaatccctt gtaattttaa cagagggtat aaggattaca cggcactacc agttggttat 3420
 gtagacaaag aatzaaata cttcccagaa accgataagg tatggattga gatggagaa 3480
 acggaaaggaa catttatogt ggacagcgtg gaattactcc ttatggagga a 3531

<210> 6
 <211> 1177
 <212> PRT
 <213> *Bacillus thuringiensis*

<400> 6
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Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
 20 25 30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
 35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
 50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
 65 70 75 80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
 85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
 100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
 115 120 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
 130 135 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
 145 150 155 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
 165 170 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
 180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
 195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
 210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
 225 230 235 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
 245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
 260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
 275 280 285

Arg Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
 290 295 300

Ile Tyr Thr Asp Ala His Arg Gly Tyr Tyr Trp Ser Gly His Gln
 305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
 325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
 340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
 355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
 370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asn Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Glu Phe Ser His Arg Leu Ser His
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445

Arg Ala Pro Thr Phe Ser Trp Gln His Arg Ser Ala Glu Phe Asn Asn
450 455 460

Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
465 470 475 480

Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
485 490 495

Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
500 505 510

Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
515 520 525

Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
530 535 540

Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
545 550 555 560

Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
565 570 575

Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
580 585 590

Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
595 600 605

Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val
610 615 620

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
625 630 635 640

Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser
645 650 655

Asp Glu Phe Cys Leu Asp Glu Lys Gln Glu Leu Ser Glu Lys Val Lys
660 665 670

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn
675 680 685

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr
690 695 700

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
705 710 715 720

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
725 730 735

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
740 745 750

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
755 760 765

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
770 775 780

Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg
785 790 795 800

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg
805 810 815

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
820 825 830

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
835 840 845

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
850 855 860

Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys
865 870 875 880

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu
885 890 895

Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
900 905 910

Val Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala Met
915 920 925

Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu
930 935 940

Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu
945 950 955 960

Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
965 970 975

Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val
980 985 990

Lys Gly His Val Asp Val Glu Glu Gln Asn Asn Gln Arg Ser Val Leu
 995 1000 1005
 Val Leu Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val
 1010 1015 1020
 Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu
 1025 1030 1035
 Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn
 1040 1045 1050
 Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Ile Tyr
 1055 1060 1065
 Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Val Asn Gln Glu
 1070 1075 1080
 Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn Arg Gly Tyr Asn Glu
 1085 1090 1095
 Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys
 1100 1105 1110
 Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys Glu Phe Asn Arg
 1115 1120 1125
 Gly Tyr Arg Asp Tyr Thr Pro Leu Pro Val Gly Tyr Val Thr Lys
 1130 1135 1140
 Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile
 1145 1150 1155
 Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu
 1160 1165 1170
 Leu Met Glu Glu
 1175

<210> 7
 <211> 3531
 <212> DNA
 <213> *Bacillus thuringiensis*

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 tcgctaacgc aatttcttt gagtgaattt gttcccggtg ctggatttgc gttaggacta 180
 gttgatataa tatgggaat tttggtccc tctcaatggg acgcatttct tgtacaaatt 240
 gaacagttaa ttaaccaaag aatagaagaa ttgcgttagga accaagccat ttcttagatta 300
 gtaggactaa gcaatcttta tcaaatttac gcagaatctt ttagagatgc ggaaggcagat 360

cctactaatac cagcattaag agaagagatg cgtattcaat tcaatgacat gaacagtgcc	420
cttacaaccg ctattccctct ttttgcagtt caaaattatac aagttccctct tttatcagta	480
tatgttcaag ctgcaaattt acatttatca gttttgagag atgtttcagt gtttggacaa	540
aggtgtggat ttgatgccgc gactatcaat agtcgttata atgatttaac taggcttatt	600
ggcaactata cagattatgc tgtacgctgg tacaatacgg gattagaacg tgtatggga	660
ccggattcta gagattgggt aaggtataat caatttagaa gagaattaac actaactgta	720
ttagatatacg ttgctctgtt cccgaattat gatagtagaa gatatccaat tcgaacagtt	780
tcccaattaa caagagaaat ttatacaaac ccagtatttag aaaattttga tggtagttt	840
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tacagaaaaa gcggaacggt agattcgctg gatgaaatac cgccacagaa taacaacgtg	1260
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gaaatttata atataattec ttcatcacaa attacacaaa tacctttaaac aaaatctact	1440
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ttacagtccg gaagctttag gactgttagt tttactactc cgtttaactt ttcaaatgga	1740
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acggattatc atattgatca agtataccat ttagttgagt gtttatcaga tgaatttgt	1980
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gagaatccctt gtgaatttaa cagagggtat agggattaca cggccactacc agttggttat 3420
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acggaaaggaa catttatcgt ggacagcgtg gaattactcc ttatggagga a 3531

<210> 8
<211> 1177
<212> PRT
<213> *Bacillus thuringiensis*

<400> 8

Met Asp Asn Asn Pro Asn Ile Asn Glu Cys Ile Pro Tyr Asn Cys Leu
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Ser Asn Pro Glu Val Glu Val Leu Gly Gly Glu Arg Ile Glu Thr Gly
20 25 30

Tyr Thr Pro Ile Asp Ile Ser Leu Ser Leu Thr Gln Phe Leu Leu Ser
35 40 45

Glu Phe Val Pro Gly Ala Gly Phe Val Leu Gly Leu Val Asp Ile Ile
50 55 60

Trp Gly Ile Phe Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile
65 70 75 80

Glu Gln Leu Ile Asn Gln Arg Ile Glu Glu Phe Ala Arg Asn Gln Ala
85 90 95

Ile Ser Arg Leu Glu Gly Leu Ser Asn Leu Tyr Gln Ile Tyr Ala Glu
100 105 110

Ser Phe Arg Glu Trp Glu Ala Asp Pro Thr Asn Pro Ala Leu Arg Glu
115 120 125

Glu Met Arg Ile Gln Phe Asn Asp Met Asn Ser Ala Leu Thr Thr Ala
130 135 140

Ile Pro Leu Phe Ala Val Gln Asn Tyr Gln Val Pro Leu Leu Ser Val
145 150 155 160

Tyr Val Gln Ala Ala Asn Leu His Leu Ser Val Leu Arg Asp Val Ser
165 170 175

Val Phe Gly Gln Arg Trp Gly Phe Asp Ala Ala Thr Ile Asn Ser Arg
180 185 190

Tyr Asn Asp Leu Thr Arg Leu Ile Gly Asn Tyr Thr Asp Tyr Ala Val
195 200 205

Arg Trp Tyr Asn Thr Gly Leu Glu Arg Val Trp Gly Pro Asp Ser Arg
210 215 220

Asp Trp Val Arg Tyr Asn Gln Phe Arg Arg Glu Leu Thr Leu Thr Val
225 230 235 240

Leu Asp Ile Val Ala Leu Phe Pro Asn Tyr Asp Ser Arg Arg Tyr Pro
245 250 255

Ile Arg Thr Val Ser Gln Leu Thr Arg Glu Ile Tyr Thr Asn Pro Val
260 265 270

Leu Glu Asn Phe Asp Gly Ser Phe Arg Gly Ser Ala Gln Gly Ile Glu
275 280 285

Gly Ser Ile Arg Ser Pro His Leu Met Asp Ile Leu Asn Ser Ile Thr
290 295 300

Ile Tyr Thr Asp Ala His Lys Gly Glu Tyr Tyr Trp Ser Gly His Gln
305 310 315 320

Ile Met Ala Ser Pro Val Gly Phe Ser Gly Pro Glu Phe Thr Phe Pro
325 330 335

Leu Tyr Gly Thr Met Gly Asn Ala Ala Pro Gln Gln Arg Ile Val Ala
340 345 350

Gln Leu Gly Gln Gly Val Tyr Arg Thr Leu Ser Ser Thr Leu Tyr Arg
355 360 365

Arg Pro Phe Asn Ile Gly Ile Asn Asn Gln Gln Leu Ser Val Leu Asp
370 375 380

Gly Thr Glu Phe Ala Tyr Gly Thr Ser Ser Asn Leu Pro Ser Ala Val
385 390 395 400

Tyr Arg Lys Ser Gly Thr Val Asp Ser Leu Asp Glu Ile Pro Pro Gln
405 410 415

Asn Asn Asn Val Pro Pro Arg Gln Gly Phe Ser His Arg Leu Ser His
420 425 430

Val Ser Met Phe Arg Ser Gly Phe Ser Asn Ser Ser Val Ser Ile Ile
435 440 445

Arg Ala Pro Thr Phe Ser Trp Gln His Arg Ser Ala Glu Phe Asn Asn
450 455 460

Ile Ile Pro Ser Ser Gln Ile Thr Gln Ile Pro Leu Thr Lys Ser Thr
465 470 475 480

Asn Leu Gly Ser Gly Thr Ser Val Val Lys Gly Pro Gly Phe Thr Gly
485 490 495

Gly Asp Ile Leu Arg Arg Thr Ser Pro Gly Gln Ile Ser Thr Leu Arg
500 505 510

Val Asn Ile Thr Ala Pro Leu Ser Gln Arg Tyr Arg Val Arg Ile Arg
515 520 525

Tyr Ala Ser Thr Thr Asn Leu Gln Phe His Thr Ser Ile Asp Gly Arg
530 535 540

Pro Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Ser Ser Gly Ser Asn
545 550 555 560

Leu Gln Ser Gly Ser Phe Arg Thr Val Gly Phe Thr Thr Pro Phe Asn
565 570 575

Phe Ser Asn Gly Ser Ser Val Phe Thr Leu Ser Ala His Val Phe Asn
580 585 590

Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val Pro Ala Glu
595 600 605

Val Thr Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Ala Val
610 615 620

Asn Glu Leu Phe Thr Ser Ser Asn Gln Ile Gly Leu Lys Thr Asp Val
625 630 635 640

Thr Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu Cys Leu Ser
645 650 655

Asp Glu Phe Cys Leu Asp Glu Lys Gln Glu Leu Ser Glu Lys Val Lys
660 665 670

His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn
675 680 685

Phe Arg Gly Ile Asn Arg Gln Leu Asp Arg Gly Trp Arg Gly Ser Thr
690 695 700

Asp Ile Thr Ile Gln Gly Gly Asp Asp Val Phe Lys Glu Asn Tyr Val
705 710 715 720

Thr Leu Leu Gly Thr Phe Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln
725 730 735

Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg
740 745 750

Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile Arg Tyr
755 760 765

Asn Ala Lys His Glu Thr Val Asn Val Pro Gly Thr Gly Ser Leu Trp
770 775 780

Pro Leu Ser Ala Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg
785 790 795 800

Cys Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser Cys Arg
805 810 815

Asp Gly Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp Ile
820 825 830

Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly Val Trp Val Ile
835 840 845

Phe Lys Ile Lys Thr Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu
850 855 860

Phe Leu Glu Glu Lys Pro Leu Val Gly Glu Ala Leu Ala Arg Val Lys
865 870 875 880

Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys Leu Glu Trp Glu
885 890 895

Thr Asn Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp Ala Leu Phe
900 905 910

Val Asn Ser Gln Tyr Asp Gln Leu Gln Ala Asp Thr Asn Ile Ala Met
915 920 925

Ile His Ala Ala Asp Lys Arg Val His Ser Ile Arg Glu Ala Tyr Leu
930 935 940

Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu
945 950 955 960

Leu Glu Gly Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala Arg Asn
965 970 975

Val Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu Ser Cys Trp Asn Val
980 985 990

Lys Gly His Val Asp Val Glu Glu Gln Asn Asn Gln Arg Ser Val Leu
995 1000 1005

Val Leu Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg Val
1010 1015 1020

Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu
1025 1030 1035

Gly Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn Asn
1040 1045 1050

Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu Glu Glu Ile Tyr
1055 1060 1065

Pro Asn Asn Thr Val Thr Cys Asn Asp Tyr Thr Val Asn Gln Glu
1070 1075 1080

Glu Tyr Gly Gly Ala Tyr Thr Ser Arg Asn Arg Gly Tyr Asn Glu
1085 1090 1095

Ala Pro Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys
1100 1105 1110

Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys Glu Phe Asn Arg
1115 1120 1125

Gly Tyr Arg Asp Tyr Thr Pro Leu Pro Val Gly Tyr Val Thr Lys
1130 1135 1140

Glu Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile Glu Ile
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Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu
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Leu Met Glu Glu
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<211> 151
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic DNA fragment used to insert point mutations into pEW3 to create the plasmid pACB-1.

<400> 9
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ccccccgagg caagaattta gtcatcgatt aagccatgtt tcaatgttta gatctggctt 120
tagtaatagt agtgtaagta taataagagc t 151

Applicant(s): David L. Edwards, Corinna Herrnstadt, Edward R. Wilcox, Siu-Fin Wong
Title: Process for Altering the Host Range of *Bacillus thuringiensis*
Toxins, and Novel Toxins Produced Thereby
Agent's File
Ref.: M12C1FDF3D2

Attorney: Saliwanchik, Lloyd & Saliwanchik

Date: January 6, 2003

Computer and
Format: IBM PC PatentIn 3.1